

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number:

10/661,809A

Source:

IFW16

Date Processed by STIC:

6/26/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 06/26/2006

PATENT APPLICATION: US/10/661,809A

TIME: 11:36:21

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\06262006\J661809A.raw

3 <110> APPLICANT: HOOK, Magnus  
 5 <120> TITLE OF INVENTION: BIOINFORMATIC METHOD FOR IDENTIFYING SURFACE-ANCHORED  
 PROTEINS FROM GRAM-  
 6 POSITIVE BACTERIA  
 8 <130> FILE REFERENCE: P07741US01/BAS  
 10 <140> CURRENT APPLICATION NUMBER: 10/661809A  
 11 <141> CURRENT FILING DATE: 2003-09-15  
 13 <150> PRIOR APPLICATION NUMBER: 60/410303  
 14 <151> PRIOR FILING DATE: 2002-09-13  
 16 <160> NUMBER OF SEQ ID NOS: 57  
 18 <170> SOFTWARE: PatentIn version 3.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 5  
 22 <212> TYPE: PRT  
 23 <213> ORGANISM: Staphylococcus epidermidis  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: MISC\_FEATURE  
 27 <222> LOCATION: (3)..(3)  
 28 <223> OTHER INFORMATION: X = any amino acid  
 31 <400> SEQUENCE: 1  
 W--> 33 Leu Pro Xaa Thr Gly  
 34 1 5  
 37 <210> SEQ ID NO: 2  
 38 <211> LENGTH: 777  
 39 <212> TYPE: PRT  
 40 <213> ORGANISM: Staphylococcus epidermidis  
 42 <400> SEQUENCE: 2  
 44 Gln Glu Gln Thr Ala Lys Glu Asp Val Ala Asp Ser Ala Thr Ser Val  
 45 1 5 10 15  
 48 Gly Ala Ile Val Ser Ile Glu Lys Ala Glu Lys Asn Phe Val Ile Thr  
 49 20 25 30  
 52 Tyr Ala Ser Gly Lys Lys Ala Gln Ile Ser Ile Leu Asn Asp His Leu  
 53 35 40 45  
 56 Phe Arg Tyr His Leu Asp Pro Thr Gly Lys Phe Glu Glu Tyr Pro Thr  
 57 50 55 60  
 60 Pro Asn Asp Pro Lys His Val Ala Lys Ile Thr Ala Lys Thr Met Ala  
 61 65 70 75 80  
 64 Asp Tyr Gly Thr Gln Ala Phe Glu Gln Thr Asn Val Thr Asp Ser Gly  
 65 85 90 95  
 68 Asn Gln Phe Ile Leu Glu Asn Asn Gly Leu Lys Ile Met Phe Glu Lys  
 69 100 105 110  
 72 Glu Ser Ala Leu Met Lys Val Leu Asp Lys Lys Lys Asn Gln Val Ile  
 73 115 120 125  
 76 Leu Glu Glu Thr Ala Pro Leu Ser Phe Lys Asn Asp Lys Ala Thr Gln

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```

77      130      135      140
80 Thr Leu Lys Gln Ser Ser Gln Glu Asn Tyr Phe Gly Gly Gly Thr Gln
81 145      150      155      160
84 Asn Gly Arg Phe Thr His Lys Gly Thr Ala Ile Gln Ile Val Asn Thr
85      165      170      175
88 Asn Asn Trp Val Asp Gly Gly Val Ala Ser Pro Asn Pro Phe Tyr Trp
89      180      185      190
92 Ser Thr Ala Gly Tyr Gly Val Val Arg Asn Thr Trp Lys Pro Gly Asn
93      195      200      205
96 Tyr Asp Phe Gly Ser His Asp Pro Gln Lys Thr Thr Thr Thr His Glu
97      210      215      220
100 Gly Thr Asp Phe Asp Ala Phe Tyr Phe Phe Asn Asp Ser Ser Ala Gly
101 225      230      235      240
104 Ile Leu Lys Asp Tyr Tyr Glu Leu Thr Gly Lys Pro Ala Leu Met Pro
105      245      250      255
108 Glu Tyr Gly Phe Tyr Glu Ala His Leu Asn Ala Tyr Asn Arg Asp Tyr
109      260      265      270
112 Trp Val Lys Val Ala Glu Gly Thr Ala Gly Ala Val Lys Phe Glu Asp
113      275      280      285
116 Gly Asn Phe Tyr Lys Glu Tyr Gln Pro Gly Asp Leu Gly Asn Leu Asn
117      290      295      300
120 Gly Thr Leu Glu Ser Leu Asn Gly Glu Lys Glu Asn Tyr Gln Phe Ser
121 305      310      315      320
124 Ala Arg Ala Val Ile Asp Arg Tyr Lys Lys Asn Asp Met Pro Leu Gly
125      325      330      335
128 Trp Phe Leu Pro Asn Asp Gly Tyr Gly Ala Gly Tyr Gly Gln Thr Asp
129      340      345      350
132 Ser Leu Asp Gly Asp Val Gln Asn Leu Lys Glu Phe Thr Glu Tyr Ala
133      355      360      365
136 Gln Ala Asn Gly Val Glu Val Gly Leu Trp Thr Gln Ser Asn Leu His
137      370      375      380
140 Pro Ala Asp Pro Lys Asn Pro Lys Lys Gly Glu Arg Asp Ile Ala Lys
141 385      390      395      400
144 Glu Val Ser Val Ala Gly Val Lys Ala Leu Lys Thr Asp Val Ala Trp
145      405      410      415
148 Val Gly Tyr Gly Tyr Ser Phe Gly Leu Asn Gly Val Glu Asp Ala Ala
149      420      425      430
152 Asn Val Phe Val Lys Glu Thr Asp Gly Ala Val Arg Pro Met Ile Val
153      435      440      445
156 Ser Leu Asp Gly Trp Ala Gly Thr Gln Arg His Ala Gly Ile Trp Thr
157      450      455      460
160 Gly Asp Gln Thr Gly Gly Gln Trp Glu Tyr Ile Arg Phe His Ile Pro
161 465      470      475      480
164 Thr Tyr Ile Gly Thr Ser Leu Ser Gly Gln Pro Asn Val Gly Ser Asp
165      485      490      495
168 Met Asp Gly Ile Phe Gly Gly Lys Asn Lys Glu Ile Asn Ile Arg Asp
169      500      505      510
172 Phe Gln Trp Lys Thr Phe Thr Pro Val Gln Leu Asn Met Asp Gly Trp
173      515      520      525

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```

176 Gly Ser Asn Pro Lys Thr Pro Phe Ala Phe Asp Gln Glu Ala Thr Asp
177      530      535      540
180 Leu Asn Arg Ala Tyr Leu Lys Leu Lys Ser Met Met Met Pro Tyr Asn
181 545      550      555      560
184 Tyr Ser Ile Ala Lys Glu Ser Val Asp Gly Leu Pro Met Val Arg Ala
185      565      570      575
188 Met Ala Leu Glu Phe Pro Asn Glu Gly Thr Ala Tyr Thr Lys Asp Ser
189      580      585      590
192 Gln Tyr Gln Tyr Met Trp Gly Pro Asn Leu Leu Val Ala Pro Ile Tyr
193      595      600      605
196 Asn Gly Asn Gln Asp Glu Ala Gly Asn Ser Ile Arg Asp Gly Ile Tyr
197      610      615      620
200 Leu Pro Asp Glu Lys Gln Val Trp Val Asp Leu Phe Thr Gly Glu Lys
201 625      630      635      640
204 Tyr Gln Gly Gly Arg Val Leu Asn Gly Val Lys Thr Pro Leu Trp Lys
205      645      650      655
208 Val Pro Val Phe Val Lys Asp Gly Ser Ile Ile Pro Met Thr Asn Pro
209      660      665      670
212 Asn Asn Asn Pro Lys Glu Phe Gln Arg Asp Gln Arg Ser Phe Leu Ile
213      675      680      685
216 Tyr Pro Asn Gly Thr Thr Ser Phe Asn Met Tyr Glu Asp Asp Gly Ile
217      690      695      700
220 Ser Thr Ser Tyr Glu Ala Gly Gln Ser Ala Thr Thr Lys Ile Asn Ser
221 705      710      715      720
224 Gln Gly Pro Lys Ser Asn Glu Lys Gly Asp Leu Thr Val Thr Ile Glu
225      725      730      735
228 Pro Thr Lys Gly Ser Tyr Lys Asp Phe Val Asp Glu Arg Ser Thr Thr
229      740      745      750
232 Leu Asp Leu Leu Ala Ser Glu Ala Pro Glu Ser Val Thr Ala Met Val
233      755      760      765
236 Gly Gly Thr Glu Val Thr Leu Lys Gln
237      770      775
240 <210> SEQ ID NO: 3
241 <211> LENGTH: 1010
242 <212> TYPE: PRT
243 <213> ORGANISM: Staphylococcus epidermidis
245 <400> SEQUENCE: 3
247 Ala Ala Asn Lys Glu Glu Phe Leu Ala Gly Thr Asn Leu Tyr Tyr Phe
248 1      5      10      15
251 Asp Lys Glu Phe Gln Val Asn Gln Tyr Leu Ser Glu Ala Ser Gly Glu
252      20      25      30
255 Lys Leu Asn Gln Ser Ala Leu Ser Val Lys Leu Ala Lys Gln Ser Val
256      35      40      45
259 Thr Ala Lys Asp Val Gln Ile Thr Val Lys Gly Phe Ile Asn Lys Gly
260      50      55      60
263 Thr Val Asp Gly Gly Asn Thr Thr Val Asp Asp Gln Leu Thr Ile Pro
264 65      70      75      80
267 Ala Asn Val Ala Ile Asn Glu Glu Lys Thr Thr Pro Ser Ser Leu Thr
268      85      90      95

```

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```

271 Leu Gln Trp Asp Gln Val Thr Glu Ala Thr Ser Tyr Glu Val Glu Arg
272      100      105      110
275 Asp Gly Thr Val Phe Gly Asn Ile Gln Thr Asn Thr Ala Thr Phe Asp
276      115      120      125
279 Gly Phe Ser Phe Leu Ser Glu His Thr Phe Arg Val Arg Ala Val Gly
280      130      135      140
283 Lys Asn Gly Val Ser Glu Trp Ser Glu Pro Ile Lys Gly Lys Thr Gln
284 145      150      155      160
287 Asp Asp Pro Tyr Lys Glu Thr Ile Asn Gln Val Lys Ala Thr Ser Asn
288      165      170      175
291 Leu Pro Glu Gln Pro Gly Ala Glu Leu Lys Lys Leu Thr Asp Lys Asp
292      180      185      190
295 Leu Ser Thr Gly Trp His Thr Asn Trp Ser Thr Gly Ile Ala Asn Pro
296      195      200      205
299 Ser Asp Gly Asn Phe Leu Ser Leu Lys Phe Asp Leu Gly Ala Glu Tyr
300      210      215      220
303 Gln Met Asp Lys Ile Glu Tyr Leu Pro Arg Asp Asn Ala Gly Asn Gly
304 225      230      235      240
307 Asn Ile Leu Gln Leu Gln Tyr Arg Thr Ser Lys Asp Gly Ala Asn Trp
308      245      250      255
311 Thr Glu Phe Ser Glu Pro Ile Asn Trp Lys Gln Asp Ala Leu Thr Lys
312      260      265      270
315 Thr Ile Glu Thr Lys Asp Gln Ala Tyr Arg Phe Val Glu Met Lys Val
316      275      280      285
319 Leu Lys Ser Val Gly Asn Phe Gly Ser Gly Arg Glu Met Leu Phe Tyr
320      290      295      300
323 Lys Gln Pro Gly Thr Glu Gly Ile Leu His Gly Asp Ile Thr Asn Asp
324 305      310      315      320
327 Gly Thr Ile Asp Glu Asn Asp Ala Met Ser Tyr Arg Asn Tyr Thr Gly
328      325      330      335
331 Leu Glu Ser Val Asp Ser Asp Phe Asn Gly Tyr Val Glu Lys Gly Asp
332      340      345      350
335 Leu Asn Lys Asn Gly Val Ile Asp Ala Tyr Asp Ile Ser Tyr Val Leu
336      355      360      365
339 Arg Gln Leu Asp Gly Gly Ile Glu Ile Pro Asp Val Glu Glu Ile Ala
340      370      375      380
343 Gly Gly Leu Ser Leu Ala Val Val Asn Glu Asn Gly Lys Asp Thr Tyr
344 385      390      395      400
347 Leu Pro Gly Asp Thr Leu Thr Phe Ile Leu Lys Gly Gln Asp Leu Lys
348      405      410      415
351 Asn Ile Asn Ala Leu Ser Thr Lys Met Ser Phe Asp Ser Ser Lys Phe
352      420      425      430
355 Glu Leu Val Gly Gln Pro Ala Thr Thr Asn Asn Thr Gln Gln Met Glu
356      435      440      445
359 Asn Tyr Ser Lys Tyr Arg Lys His Ser Asn Asp Val Glu Asn Leu Tyr
360      450      455      460
363 Leu Val Leu Ser Asn Gln Gly Asn Lys Gln Leu Leu Asn Gly Ser Met
364 465      470      475      480
367 Asp Leu Val Thr Phe Lys Val Lys Val Lys Glu Thr Thr Arg Val Lys

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```

368          485          490          495
371 Arg Ala Thr Thr Val Glu Gln Pro Leu Gln Phe Asp Met Ser Gln Gly
372          500          505          510
375 Leu Leu Val Gly Gln Gly Phe Gln Gln Ala Thr Leu Ser Asp Phe Ser
376          515          520          525
379 Val Thr Val Lys Pro Thr Glu Leu Val Asp Lys Glu Leu Leu Gln Ala
380          530          535          540
383 Leu Ile Thr Leu Asn Gln Ala Arg Val Glu Lys Glu Tyr Thr Pro Glu
384 545          550          555          560
387 Thr Trp Ala Ile Phe Lys Pro Ile Leu Asp Glu Ala Val Ala Val Leu
388          565          570          575
391 Ala Asn Glu Gln Ala Thr Gln Thr Asp Val Ser Ala Ala Ala Glu Asn
392          580          585          590
395 Leu Glu Lys Ala Ala Ser Gln Leu Glu Lys Met Pro Asp Val Ala Asn
396          595          600          605
399 Lys Ala Asp Leu Glu Lys Ala Ile Gln Glu Gly Leu Ala Lys Lys Pro
400          610          615          620
403 Ser Asp Gly Gln Glu Phe Thr Glu Glu Thr Lys Lys Val Leu Glu Glu
404 625          630          635          640
407 Ser Leu Ala Ala Ala Gln Lys Val Phe Ala Gln Glu Lys Val Thr Gln
408          645          650          655
411 Glu Glu Ile Asp Gln Ala Thr Lys Thr Leu Arg Glu Ala Ile Ala Gln
412          660          665          670
415 Leu Lys Glu Gln Pro Val Ala Val Asp Lys Glu Thr Leu Lys Glu Gln
416          675          680          685
419 Ile Ala Gln Ala Arg Gly Arg Lys Pro Glu Glu Gly Tyr Gln Phe Thr
420          690          695          700
423 Lys Glu Thr Glu Lys Gln Leu Gln Glu Ala Ile Gln Ala Ala Glu Ala
424 705          710          715          720
427 Ile Val Ala Lys Glu Thr Ala Thr Lys Glu Glu Val Ser Glu Ala Leu
428          725          730          735
431 Asn Ala Leu Glu Thr Ala Met Ala Gln Leu Lys Glu Val Pro Leu Val
432          740          745          750
435 Asn Lys Asp Gln Leu Gln Glu Val Val Lys Arg Ala Gln Gln Val Thr
436          755          760          765
439 Pro Ser Glu Gly His Gln Phe Thr Ala Ser Ser Leu Gln Glu Leu Gln
440          770          775          780
443 Lys Ala Leu Leu Ala Ala Lys Asn Thr Leu Lys Asn Pro Ala Ala Asn
444 785          790          795          800
447 Gln Lys Met Ile Asp Glu Ala Val Ala Glu Leu Thr Ser Ala Ile Asp
448          805          810          815
451 Gly Leu Gln Glu Glu Val Leu Val Thr Asp Lys Lys Ala Leu Glu Ala
452          820          825          830
455 Met Ile Ala Lys Ala Lys Ala Ile Lys Pro Ser Ala Gly Lys Glu Phe
456          835          840          845
459 Thr Ser Glu Ser Lys Ala Arg Leu Thr Glu Ala Ile Asp Gln Ala Glu
460          850          855          860
463 Gly Ile Leu Ala Asp Lys Asn Ala Arg Gln Glu Gln Ile Asp Ile Ala
464 865          870          875          880

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/661,809A

DATE: 06/26/2006  
TIME: 11:36:22

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\06262006\J661809A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 3

Seq#:25; Xaa Pos. 3

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

**VERIFICATION SUMMARY**

**PATENT APPLICATION: US/10/661,809A**

**DATE: 06/26/2006**

**TIME: 11:36:22**

**Input Set : A:\PTO.DA.txt**

**Output Set: N:\CRF4\06262006\J661809A.raw**

**L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0**

**L:7682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0**